

SEQUENCE LISTING

<110> Lehar, Sophie
Manning, Stephen
Coyle, Anthony J.
Gutierrez-Ramos, Jose-Carlos

<120> Novel Th2-Specific Molecules and Uses Thereof

<130> 5800-10B

<140>

<141>

<150> 09/168,229

<151> 1998-10-07

<150> 09/258,670

<151> 1999-02-26

<160> 24

<170> PatentIn Ver. 2.0

<210> 1

<211> 3631

<212> DNA

<213> Mus sp.

<220>

<221> CDS

<222> (126)..(1304)

<400> 1

```
ccacgcgtcc gcggaacgcgt gggcgggaaa ggaatcctgg ggttttctag tatccccttc 60
tttttttctt ttttcttttc tttttctttt tggccctgcg ggcttcagac tcaggggaact 120
tgctc atg gct ttt ttg atg aag aag aag aaa ttt aaa ttt caa acc act 170
      Met Ala Phe Leu Met Lys Lys Lys Lys Phe Lys Phe Gln Thr Thr
        1             5             10             15

ttc acc ttg gag gag ctg act gcg gtc ccc ttc gtg aac ggg gtc ctc 218
Phe Thr Leu Glu Glu Leu Thr Ala Val Pro Phe Val Asn Gly Val Leu
              20              25              30

ttt tgc aag gtc cgg ctg ctg gat ggc ggg gat ttt gtc agc ttg tcg 266
Phe Cys Lys Val Arg Leu Leu Asp Gly Gly Asp Phe Val Ser Leu Ser
              35              40              45

tcc agg gag gag gtg cag gag aac tgt gta cga tgg cgg aag agg ttc 314
Ser Arg Glu Glu Val Gln Glu Asn Cys Val Arg Trp Arg Lys Arg Phe
        50              55              60
```

acc ttt gtg tgt aaa atg agt gcc aac ccg gcc aca ggc ctg ctg gac	362
Thr Phe Val Cys Lys Met Ser Ala Asn Pro Ala Thr Gly Leu Leu Asp	
65 70 75	
ccc tgc atc ttt cga gtg tct gtg cgc aag gag ctg aaa ggt ggg aag	410
Pro Cys Ile Phe Arg Val Ser Val Arg Lys Glu Leu Lys Gly Gly Lys	
80 85 90 95	
gcg tat tcc aag ctg ggc ttc act gac ttg aac cta gcc gag ttt gca	458
Ala Tyr Ser Lys Leu Gly Phe Thr Asp Leu Asn Leu Ala Glu Phe Ala	
100 105 110	
ggc tca ggc tcc acc gtc cgc tgc tgc cta ttg gaa gga tac gac acc	506
Gly Ser Gly Ser Thr Val Arg Cys Cys Leu Leu Glu Gly Tyr Asp Thr	
115 120 125	
aag aat acc cgc cag gac aac tcc atc ctc aag gtc acc att ggc atg	554
Lys Asn Thr Arg Gln Asp Asn Ser Ile Leu Lys Val Thr Ile Gly Met	
130 135 140	
ttc ctg ctc tct ggg gac ccc tgt ttc aag acg cca ccg tct acc gcc	602
Phe Leu Leu Ser Gly Asp Pro Cys Phe Lys Thr Pro Pro Ser Thr Ala	
145 150 155	
aaa tcc atc tcc atc ccg ggc cag gac tcc tcc ctg cag ctg acg tgt	650
Lys Ser Ile Ser Ile Pro Gly Gln Asp Ser Ser Leu Gln Leu Thr Cys	
160 165 170 175	
aaa ggt ggt ggg acc agc agc ggt ggc agc agc agc acc aat tcc cta	698
Lys Gly Gly Gly Thr Ser Ser Gly Gly Ser Ser Ser Thr Asn Ser Leu	
180 185 190	
act gga tcc cgg ccc ccc aag acc cgg ccc acc atc ctg ggc tca gga	746
Thr Gly Ser Arg Pro Pro Lys Thr Arg Pro Thr Ile Leu Gly Ser Gly	
195 200 205	
cta cca gag gag cca gac cag agc ctg tcc agt cct gag gag gtg ttc	794
Leu Pro Glu Glu Pro Asp Gln Ser Leu Ser Ser Pro Glu Glu Val Phe	
210 215 220	
cac tct ggc cac tcc cgc aac tcc agc tat gcc agc cag cag tcc aag	842
His Ser Gly His Ser Arg Asn Ser Ser Tyr Ala Ser Gln Gln Ser Lys	
225 230 235	
cta tct ggc tac agt aca gag cac tct cgc tcc tcc agc ctg tct gac	890
Leu Ser Gly Tyr Ser Thr Glu His Ser Arg Ser Ser Ser Leu Ser Asp	
240 245 250 255	
ttg aca cac cgc aga aat aca tcc acc agc agc agc gcc tct ggt ggc	938
Leu Thr His Arg Arg Asn Thr Ser Thr Ser Ser Ser Ala Ser Gly Gly	
260 265 270	
ctc agt atg gct gta gag ggt cct gag ggc atg gag agg gag cat cgg	986
Leu Ser Met Ala Val Glu Gly Pro Glu Gly Met Glu Arg Glu His Arg	

275	280	285
ccc tct gag aag cca cct cgg cct cct gag aag ccc cca cgc ccc cca 1034		
Pro Ser Glu Lys Pro Pro Arg Pro Pro Glu Lys Pro Pro Arg Pro Pro 290 295 300		
cgc ccc ttg cat cta tca gat cgc tct ttt cgg cga aag aaa gac tct 1082		
Arg Pro Leu His Leu Ser Asp Arg Ser Phe Arg Arg Lys Lys Asp Ser 305 310 315		
gtg gag agc cac cca acc tgg gta gat gac act cga att gat gca gac 1130		
Val Glu Ser His Pro Thr Trp Val Asp Asp Thr Arg Ile Asp Ala Asp 320 325 330 335		
gac att gtg gag aag ata atg cag agc cag gac ttc act gat ggc agc 1178		
Asp Ile Val Glu Lys Ile Met Gln Ser Gln Asp Phe Thr Asp Gly Ser 340 345 350		
aac act gag gac agt aac ctt cgg ctg ttc gtg agc cgt gat ggc tcc 1226		
Asn Thr Glu Asp Ser Asn Leu Arg Leu Phe Val Ser Arg Asp Gly Ser 355 360 365		
acc aca ctg agc ggc att cag ctg ggc aac aga gtc tcc tcg gga gtc 1274		
Thr Thr Leu Ser Gly Ile Gln Leu Gly Asn Arg Val Ser Ser Gly Val 370 375 380		
tac gag cca gtc gta att gag agc cac tga gggacccagg agtccggctg 1324		
Tyr Glu Pro Val Val Ile Glu Ser His 385 390		
aagaagggtc ctgccatctc tggcaccag gcccgaggca ttctggagg atctgctctg 1384		
cattgcatct gtgcctctc ttactctagc cacactggcc ccaaagcgt cattccattt 1444		
tcctcccatc caccctggaa ccaactgggtc tgggtgccac tgtgaatatt gtcctccgaa 1504		
ccactagaaa atggggcaag atggagctgg ccaggactgc cctgactgga gaggacctgg 1564		
gccagcaaaa ggacacagcc attccatggt ggggtgcttgt ggcctgcccc atccctccat 1624		
ccccacgac ccacttcagg agcagcagct tcagccaggc tgacgggggca cttgctccat 1684		

tgtccctgcc cttcacgagc tggggccaccc cagaaccctg ccacctgtga ccctctgctt
1744

actgcttcac tgtcttttct ctatcctgag gagacctgca ggcagctctc tcctggggagc
1804

taagacctca aacccacac tctggattga gacccacct ccttaactgt cctcctgctg
1864

ccctgcagcc tgcactttgc acatgcttgt cccagcaca gccaccggcc cttgcccttc
1924

tccagacctc ctgggtgctg tctgctgtgc aaccagacct aggggtacagt cgccccgctg
1984

gaactgtggca ctacccttc cctctaatta accccaaact cagaccaag accggagcct
2044

agaagggcct gagcatcatg gttccatctg cccagggctg ggtcctgagc agctggcctt
2104

cctgcaggaa aggaaggacg aggccagcc gtgctgggta agcaaaggcc ttttccccct
2164

gctctcatgt cagccggcct gggctgggtt ccaggctaga gagtcagcca ggtggcctgt
2224

gactgggtga actggagctg gcttcctgcc agacgagcct cagccctcct gggcaagggg
2284

tgtgctttcc ctggggagtc ttccccctac tactcacct cttggtacct ccccaacccc
2344

agcactttct gtccataat ttgcttaagg agagtatagg ctgccagctc agccctggat
2404

aaattccac ccccttaagt ttcactcact tcgtatcaac ccagcaggct ggtgtttcct
2464

tggcccccta aggtgttttt cctcctgagt tcacagttct tgtattcctt ccacccaac
2524

aaggggagat aggtgcctct gttccccatt ccacctgcac ccagcaggg ctggggatag
2584

gcgagtatgg gacattgttt ctgtgggtgg ggatggctgg actccccagg ttgggaaggt
2644

ccttgccatg tttgtgtctt cctcagctag caaaagttgg ggctgtggtc ttggagctgc
2704

ctgggtgtcag gaccagatca tttctatagg ttctgtagcc gttgttttaa tcagcagatg
2764

aatgttagaa gatgctgcca aggcaaggca gaacatggct agagaagggt ccggcagctc
2824

agattccatc ctgcccagca ggtgcctggc actttaaggg actctggcag ctctgttctt
2884

aggtgaggtg accaccagaa gatggacaga gccctagtgt gcttgtctac taccttcccc
2944

agtcagcatt gttttgggtct agttctaaat tccagggctc caaaccaagc agttgggtact
3004

gtcaggaaga ctgccccaaa ccaagagccc ctgcctaact caagccaagg tctgggactg
3064

gatggccact ccagtagacg agagctgcca catcctctgc ttccaggcac tgggccagga
3124

taacttagct gaaaacatga ccacaaccaa atgaacactg gtggcagcca gaggctaaga
3184

gccttttctc ctgcgctcag tgatccccac gggtgcccag agcacctgga cttcaaattc
3244

tatatacaaa gatagaggat atattagagg tatttttgaa aaggaattgg tctatgcaat
3304

gccagtttgg gacctgtaag acagtttaat gtttctatta gagagatata aaagatctgc
3364

aatattttta gggttctttt ctgggttacc tacagctgac cacgtgggtct ggcaggatga
3424

gcaggcccat cttcttctgt ggggagaatt tgcttttgtg ttattccttt ctaaccaggt
3484

taccactgca ccccatccg tgggctgttc atatctgtct cagcttataa tagaaaatta
3544

tgatcatatgg ggaaatcagc ctagtgtcaa tgtttggttt ggggggtggaa ttaaagtccg
3604

atgtttttgt taaaaaaaaa aaaaaaa
3631

<210> 2
<211> 392
<212> PRT
<213> Mus sp.

<400> 2
Met Ala Phe Leu Met Lys Lys Lys Lys Phe Lys Phe Gln Thr Thr Phe

1		5		10		15													
Thr	Leu	Glu	Glu	Leu	Thr	Ala	Val	Pro	Phe	Val	Asn	Gly	Val	Leu	Phe				
			20					25					30						
Cys	Lys	Val	Arg	Leu	Leu	Asp	Gly	Gly	Asp	Phe	Val	Ser	Leu	Ser	Ser				
		35					40					45							
Arg	Glu	Glu	Val	Gln	Glu	Asn	Cys	Val	Arg	Trp	Arg	Lys	Arg	Phe	Thr				
	50					55					60								
Phe	Val	Cys	Lys	Met	Ser	Ala	Asn	Pro	Ala	Thr	Gly	Leu	Leu	Asp	Pro				
65					70					75					80				
Cys	Ile	Phe	Arg	Val	Ser	Val	Arg	Lys	Glu	Leu	Lys	Gly	Gly	Lys	Ala				
				85					90					95					
Tyr	Ser	Lys	Leu	Gly	Phe	Thr	Asp	Leu	Asn	Leu	Ala	Glu	Phe	Ala	Gly				
			100					105					110						
Ser	Gly	Ser	Thr	Val	Arg	Cys	Cys	Leu	Leu	Glu	Gly	Tyr	Asp	Thr	Lys				
		115					120					125							
Asn	Thr	Arg	Gln	Asp	Asn	Ser	Ile	Leu	Lys	Val	Thr	Ile	Gly	Met	Phe				
		130				135					140								
Leu	Leu	Ser	Gly	Asp	Pro	Cys	Phe	Lys	Thr	Pro	Pro	Ser	Thr	Ala	Lys				
145					150					155					160				
Ser	Ile	Ser	Ile	Pro	Gly	Gln	Asp	Ser	Ser	Leu	Gln	Leu	Thr	Cys	Lys				
				165					170					175					
Gly	Gly	Gly	Thr	Ser	Ser	Gly	Gly	Ser	Ser	Ser	Thr	Asn	Ser	Leu	Thr				
			180					185					190						
Gly	Ser	Arg	Pro	Pro	Lys	Thr	Arg	Pro	Thr	Ile	Leu	Gly	Ser	Gly	Leu				
		195					200					205							
Pro	Glu	Glu	Pro	Asp	Gln	Ser	Leu	Ser	Ser	Pro	Glu	Glu	Val	Phe	His				
	210					215					220								
Ser	Gly	His	Ser	Arg	Asn	Ser	Ser	Tyr	Ala	Ser	Gln	Gln	Ser	Lys	Leu				
225					230				235						240				
Ser	Gly	Tyr	Ser	Thr	Glu	His	Ser	Arg	Ser	Ser	Ser	Leu	Ser	Asp	Leu				
				245					250					255					
Thr	His	Arg	Arg	Asn	Thr	Ser	Thr	Ser	Ser	Ser	Ala	Ser	Gly	Gly	Leu				
			260				265						270						
Ser	Met	Ala	Val	Glu	Gly	Pro	Glu	Gly	Met	Glu	Arg	Glu	His	Arg	Pro				
	275						280					285							
Ser	Glu	Lys	Pro	Pro	Arg	Pro	Pro	Glu	Lys	Pro	Pro	Arg	Pro	Pro	Arg				

ttc tgg aat gac atc aac cag tgt gga aga aga gac tgt gcc gtc aaa	341
Phe Trp Asn Asp Ile Asn Gln Cys Gly Arg Arg Asp Cys Ala Val Lys	
90 95 100	
ccc tgc cat tct gat gaa gtt cct gat gga att aag tct gcg agc tac	389
Pro Cys His Ser Asp Glu Val Pro Asp Gly Ile Lys Ser Ala Ser Tyr	
105 110 115	
aag tat tct gag gaa gcc aac cgc att gaa gaa tgt gag caa gct gag	437
Lys Tyr Ser Glu Glu Ala Asn Arg Ile Glu Glu Cys Glu Gln Ala Glu	
120 125 130	
cga ctt gga gcc gtg gat gag tct ctg agt gag gag acc cag aaa gct	485
Arg Leu Gly Ala Val Asp Glu Ser Leu Ser Glu Glu Thr Gln Lys Ala	
135 140 145 150	
gta ctt cag tgg acc aag cat gat gat tgc tca gac agc ttc tgc gaa	533
Val Leu Gln Trp Thr Lys His Asp Asp Ser Ser Asp Ser Phe Cys Glu	
155 160 165	
att gac gat ata cag tcc ccc gat gct gag tat gtg gac tta ctc ctt	581
Ile Asp Asp Ile Gln Ser Pro Asp Ala Glu Tyr Val Asp Leu Leu Leu	
170 175 180	
aac cct gag cgc tac aca ggc tac aag ggg cca gac gct tgg agg ata	629
Asn Pro Glu Arg Tyr Thr Gly Tyr Lys Gly Pro Asp Ala Trp Arg Ile	
185 190 195	
tgg agt gtc atc tat gaa gaa aac tgt ttt aag cca cag aca att caa	677
Trp Ser Val Ile Tyr Glu Glu Asn Cys Phe Lys Pro Gln Thr Ile Gln	
200 205 210	
agg cct ttg gct tct ggg cga gga aaa agt aaa gag aac aca ttt tac	725
Arg Pro Leu Ala Ser Gly Arg Gly Lys Ser Lys Glu Asn Thr Phe Tyr	
215 220 225 230	
aac tgg cta gaa ggc ctc tgt gta gaa aag aga gca ttc tac aga ctt	773
Asn Trp Leu Glu Gly Leu Cys Val Glu Lys Arg Ala Phe Tyr Arg Leu	
235 240 245	
ata tct ggc ctg cac gca agc att aat gtg cat ttg agt gca agg tat	821
Ile Ser Gly Leu His Ala Ser Ile Asn Val His Leu Ser Ala Arg Tyr	
250 255 260	
ctt tta caa gat act tgg ctg gaa aag aaa tgg ggt cac aat gtc aca	869
Leu Leu Gln Asp Thr Trp Leu Glu Lys Lys Trp Gly His Asn Val Thr	
265 270 275	
gag ttc cag cag cgc ttt gat ggg att ctg act gaa gga gaa ggc cca	917
Glu Phe Gln Gln Arg Phe Asp Gly Ile Leu Thr Glu Gly Glu Gly Pro	
280 285 290	
cga agg ctg agg aac ttg tac ttc ctg tac ctg ata gag tta agg gct	965

Arg Arg Leu Arg Asn Leu Tyr Phe Leu Tyr Leu Ile Glu Leu Arg Ala
 295 300 305 310

ctc tcc aaa gtg ctt cca ttt ttt gag cgt cca gat ttt cag ctc ttc
 1013

Leu Ser Lys Val Leu Pro Phe Phe Glu Arg Pro Asp Phe Gln Leu Phe
 315 320 325

act ggg aat aaa gtt cag gat gca gaa aac aaa gcg tta ctt ctg gag
 1061

Thr Gly Asn Lys Val Gln Asp Ala Glu Asn Lys Ala Leu Leu Leu Glu
 330 335 340

ata ctt cat gaa atc aag tca ttt cct ttg cac ttc gat gag aat tct
 1109

Ile Leu His Glu Ile Lys Ser Phe Pro Leu His Phe Asp Glu Asn Ser
 345 350 355

ttt ttt gct ggg gat aaa aac gaa gca cat aaa cta aag gag gac ttc
 1157

Phe Phe Ala Gly Asp Lys Asn Glu Ala His Lys Leu Lys Glu Asp Phe
 360 365 370

cgg cta cac ttt agg aac att tca aga atc atg gac tgt gtt ggc tgc
 1205

Arg Leu His Phe Arg Asn Ile Ser Arg Ile Met Asp Cys Val Gly Cys
 375 380 385 390

ttc aag tgc cgc ctg tgg ggc aag ctt cag acg cag ggg ctg ggc act
 1253

Phe Lys Cys Arg Leu Trp Gly Lys Leu Gln Thr Gln Gly Leu Gly Thr
 395 400 405

gct ctg aag atc ttg ttt tcc gaa aaa ctg atc gca aat atg ccg gaa
 1301

Ala Leu Lys Ile Leu Phe Ser Glu Lys Leu Ile Ala Asn Met Pro Glu
 410 415 420

agc gga cca agt tat gag ttc cag cta acc aga caa gaa ata gta tca
 1349

Ser Gly Pro Ser Tyr Glu Phe Gln Leu Thr Arg Gln Glu Ile Val Ser
 425 430 435

ctg ttt aat gca ttt gga agg att tcc aca agt gtg aga gaa cta gag
 1397

Leu Phe Asn Ala Phe Gly Arg Ile Ser Thr Ser Val Arg Glu Leu Glu
 440 445 450

aac ttc agg cac ttg tta cag aat gtt cac tga ggaggacggt tggaatgtgc
 1450

Asn Phe Arg His Leu Leu Gln Asn Val His
 455 460 465

Lys Pro Gln Thr Ile Gln Arg Pro Leu Ala Ser Gly Arg Gly Lys Ser
210 215 220

Lys Glu Asn Thr Phe Tyr Asn Trp Leu Glu Gly Leu Cys Val Glu Lys
225 230 235 240

Arg Ala Phe Tyr Arg Leu Ile Ser Gly Leu His Ala Ser Ile Asn Val
245 250 255

His Leu Ser Ala Arg Tyr Leu Leu Gln Asp Thr Trp Leu Glu Lys Lys
260 265 270

Trp Gly His Asn Val Thr Glu Phe Gln Gln Arg Phe Asp Gly Ile Leu
275 280 285

Thr Glu Gly Glu Gly Pro Arg Arg Leu Arg Asn Leu Tyr Phe Leu Tyr
290 295 300

Leu Ile Glu Leu Arg Ala Leu Ser Lys Val Leu Pro Phe Phe Glu Arg
305 310 315 320

Pro Asp Phe Gln Leu Phe Thr Gly Asn Lys Val Gln Asp Ala Glu Asn
325 330 335

Lys Ala Leu Leu Leu Glu Ile Leu His Glu Ile Lys Ser Phe Pro Leu
340 345 350

His Phe Asp Glu Asn Ser Phe Phe Ala Gly Asp Lys Asn Glu Ala His
355 360 365

Lys Leu Lys Glu Asp Phe Arg Leu His Phe Arg Asn Ile Ser Arg Ile
370 375 380

Met Asp Cys Val Gly Cys Phe Lys Cys Arg Leu Trp Gly Lys Leu Gln
385 390 395 400

Thr Gln Gly Leu Gly Thr Ala Leu Lys Ile Leu Phe Ser Glu Lys Leu
405 410 415

Ile Ala Asn Met Pro Glu Ser Gly Pro Ser Tyr Glu Phe Gln Leu Thr
420 425 430

Arg Gln Glu Ile Val Ser Leu Phe Asn Ala Phe Gly Arg Ile Ser Thr
435 440 445

Ser Val Arg Glu Leu Glu Asn Phe Arg His Leu Leu Gln Asn Val His
450 455 460

<210> 5
<211> 4382
<212> DNA
<213> Mus sp.

```

<220>
<221> CDS
<222> (36)..(1430)

<400> 5
cggcgcgggt agagggcggt gggcggcgag cggcgc atg ggc cgc gcc tgg ggc 53
                               Met Gly Arg Ala Trp Gly
                               1           5

ttg ctc gtt gga ctc ctg ggc gtc gtg tgg ctg ctg cgc ttg ggc cac 101
Leu Leu Val Gly Leu Leu Gly Val Val Trp Leu Leu Arg Leu Gly His
                10                15                20

ggc gag gag cgg cgg ccg gag aca gcg gca cag cgc tgc ttc tgc cag 149
Gly Glu Glu Arg Arg Pro Glu Thr Ala Ala Gln Arg Cys Phe Cys Gln
                25                30                35

gtt agt ggt tac ctg gac gac tgt acc tgt gat gtc gag acc atc gat 197
Val Ser Gly Tyr Leu Asp Asp Cys Thr Cys Asp Val Glu Thr Ile Asp
                40                45                50

aag ttt aat aac tac aga ctt ttc cca aga cta caa aag ctt ctt gaa 245
Lys Phe Asn Asn Tyr Arg Leu Phe Pro Arg Leu Gln Lys Leu Leu Glu
                55                60                65                70

agt gac tac ttt aga tat tac aag gtg aac ttg aag aag cct tgt cct 293
Ser Asp Tyr Phe Arg Tyr Tyr Lys Val Asn Leu Lys Lys Pro Cys Pro
                75                80                85

ttc tgg aat gac atc aac cag tgt gga aga aga gac tgt gcc gtc aaa 341
Phe Trp Asn Asp Ile Asn Gln Cys Gly Arg Arg Asp Cys Ala Val Lys
                90                95                100

ccc tgc cat tct gat gaa gtt cct gat gga att aag tct gcg agc tac 389
Pro Cys His Ser Asp Glu Val Pro Asp Gly Ile Lys Ser Ala Ser Tyr
                105                110                115

aag tat tct gag gaa gcc aac cgc att gaa gaa tgt gag caa gct gag 437
Lys Tyr Ser Glu Glu Ala Asn Arg Ile Glu Glu Cys Glu Gln Ala Glu
                120                125                130

cga ctt gga gcc gtg gat gag tct ctg agt gag gag acc cag aaa gct 485
Arg Leu Gly Ala Val Asp Glu Ser Leu Ser Glu Glu Thr Gln Lys Ala
                135                140                145                150

gta ctt cag tgg acc aag cat gat gat tcg tca gac agc ttc tgc gaa 533
Val Leu Gln Trp Thr Lys His Asp Asp Ser Ser Asp Ser Phe Cys Glu
                155                160                165

att gac gat ata cag tcc ccc gat gct gag tat gtg gac tta ctc ctt 581
Ile Asp Asp Ile Gln Ser Pro Asp Ala Glu Tyr Val Asp Leu Leu Leu
                170                175                180

```

aac cct gag cgc tac aca ggc tac aag ggg cca gac gct tgg agg ata	629
Asn Pro Glu Arg Tyr Thr Gly Tyr Lys Gly Pro Asp Ala Trp Arg Ile	
185 190 195	
tgg agt gtc atc tat gaa gaa aac tgt ttt aag cca cag aca att caa	677
Trp Ser Val Ile Tyr Glu Glu Asn Cys Phe Lys Pro Gln Thr Ile Gln	
200 205 210	
agg cct ttg gct tct ggg cga gga aaa agt aaa gag aac aca ttt tac	725
Arg Pro Leu Ala Ser Gly Arg Gly Lys Ser Lys Glu Asn Thr Phe Tyr	
215 220 225 230	
aac tgg cta gaa ggc ctc tgt gta gaa aag aga gca ttc tac aga ctt	773
Asn Trp Leu Glu Gly Leu Cys Val Glu Lys Arg Ala Phe Tyr Arg Leu	
235 240 245	
ata tct ggc ctg cac gca agc att aat gtg cat ttg agt gca agg tat	821
Ile Ser Gly Leu His Ala Ser Ile Asn Val His Leu Ser Ala Arg Tyr	
250 255 260	
ctt tta caa gat act tgg ctg gaa aag aaa tgg ggt cac aat gtc aca	869
Leu Leu Gln Asp Thr Trp Leu Glu Lys Lys Trp Gly His Asn Val Thr	
265 270 275	
gag ttc cag cag cgc ttt gat ggg att ctg act gaa gga gaa ggc cca	917
Glu Phe Gln Gln Arg Phe Asp Gly Ile Leu Thr Glu Gly Glu Gly Pro	
280 285 290	
cga agg ctg agg aac ttg tac ttc ctg tac ctg ata gag tta agg gct	965
Arg Arg Leu Arg Asn Leu Tyr Phe Leu Tyr Leu Ile Glu Leu Arg Ala	
295 300 305 310	
ctc tcc aaa gtg ctt cca ttt ttt gag cgt cca gat ttt cag ctc ttc	
1013	
Leu Ser Lys Val Leu Pro Phe Phe Glu Arg Pro Asp Phe Gln Leu Phe	
315 320 325	
act ggg aat aaa gtt cag gat gca gaa aac aaa gcg tta ctt ctg gag	
1061	
Thr Gly Asn Lys Val Gln Asp Ala Glu Asn Lys Ala Leu Leu Leu Glu	
330 335 340	
ata ctt cat gaa atc aag tca ttt cct ttg cac ttc gat gag aat tct	
1109	
Ile Leu His Glu Ile Lys Ser Phe Pro Leu His Phe Asp Glu Asn Ser	
345 350 355	
ttt ttt gct ggg gat aaa aac gaa gca cat aaa cta aag gag gac ttc	
1157	
Phe Phe Ala Gly Asp Lys Asn Glu Ala His Lys Leu Lys Glu Asp Phe	
360 365 370	
cgg cta cac ttt agg aac att tca aga atc atg gac tgt gtt ggc tgc	
1205	

Arg Leu His Phe Arg Asn Ile Ser Arg Ile Met Asp Cys Val Gly Cys
 375 380 385 390

ttc aag tgc cgc ctg tgg ggc aag ctt cag acg cag ggg ctg ggc act
 1253

Phe Lys Cys Arg Leu Trp Gly Lys Leu Gln Thr Gln Gly Leu Gly Thr
 395 400 405

gct ctg aag atc ttg ttt tcc gaa aaa ctg atc gca aat atg ccg gaa
 1301

Ala Leu Lys Ile Leu Phe Ser Glu Lys Leu Ile Ala Asn Met Pro Glu
 410 415 420

agc gga cca agt tat gag ttc cag cta acc aga caa gaa ata gta tca
 1349

Ser Gly Pro Ser Tyr Glu Phe Gln Leu Thr Arg Gln Glu Ile Val Ser
 425 430 435

ctg ttt aat gca ttt gga agg att tcc aca agt gtg aga gaa cta gag
 1397

Leu Phe Asn Ala Phe Gly Arg Ile Ser Thr Ser Val Arg Glu Leu Glu
 440 445 450

aac ttc agg cac ttg tta cag aat gtt cac tga ggaggacggt tggaatgtgc
 1450

Asn Phe Arg His Leu Leu Gln Asn Val His
 455 460 465

ctgtttctgc acaggggaat ctgaaggga gaatctctct gagcaccatg gttgcaatga
 1510

ctgtcctaag ccaaacgttt atataaagct gcttttgtaa aagaagagat acattgtctt
 1570

aagtaaatga cattttttaa aattgtgttc atgtttaata ttattgtgaa tagaagtagt
 1630

attttgataa tatacaaatt ttaatactaa gcaaaagtaa ggtcattaaa ctcccttatg
 1690

ataaagctag gtaaattattg ccttaggctc tcaaactaga gttgaattta agaaggtaat
 1750

gaaagctaag ctaagggtacc tgtgacaagt gtttggtaat aaaatactaa gaggctcagc
 1810

agtaaaccat gggtatcagc ctcagatacc aatgcttttt catttgcttc atatacaaag
 1870

aaaatacaga ctgcccagtt agatttaagt tttagaaaag caaccagttt tcctttcaat
 1930

gttaagtgtg ttgaagttta ttagggccta ttatactac aagttatttg ctggaagttc
 1990

aagtttaact gggagccctg tgttttcctg gcaaccttaa aatacactgg tatgaaacat
2050

tccttttaga gttaaatagc tattttgatt gtgctgtttt ggtatgttgg gaagtagaac
2110

aattcaaagg cacaggagat ttctaaacat cgtagaaaga taaatagatt atatatttat
2170

tctcataata gtttccctaa tggaattttg gggaaaattt tatttttata taatttcata
2230

tttacagaaa agtttcaaaa acagttaaaa aaaaaaccaa actggtttta ctcagattca
2290

tggattgttc acatgtgttt taaccctca cccagctca gagtggcgat tgagcccagg
2350

acctcagtca tgctgggcta gcctgcatt catgagctgt gtctcaggc cttgcttaag
2410

ctcctacata gacatagaca ccctgttttt atttaagggg ttgagtcatg ggcctcatga
2470

tttaacccaa aatacttcag tgtgggtggtc aataatttcc taaaaactat tttttgtttt
2530

ctttttaaag gaatatccaa accttacaaa tctgagctga actacttact ataagcctta
2590

aaataagggg gacatccac atcccagcca cctgacgttt gaatttggtt gcctttttcg
2650

acctgtgtag tcacaggcta tacaactcat gtttttacgc atgaaactct gtttttctcc
2710

acaggatgga gctgtaacgt agataggatg ggttggttagt agaagctcta cactgagagc
2770

agtatttgat gtggcttaag aatttacatc acatggcaat tataaatggc atatacctca
2830

aaattatgcc cccttgaggc cacatctaata gtcttgagca gttaggactg gttgagatgt
2890

cacataagaa aaagcaggac ttacgtatgt aatggctagg aatgtcactt tacactgttg
2950

tgtattttct ctgtccctaa gacttggctc agtgccaggc atacagttgg tgtctaatat
3010

ttattgatgg aaagtatatg tatttagtat acgttaagtg atgggtgatgt agcttggtta
3070

gtaatgtatc ctatttcccc ctccctctca ctttttcttt tggatctcat aataaaagac
3130

atcaaccac taattaggtc agttttcttg gggacttaaa agaactaaag tgatcaccac
3190

acacaagcca gcccttttga aaccctcact gctttcacgt gcttttccca cttgattggc
3250

tatgtcctct gtccttccaa gtgaagtcta atacctaatt ctaagtttat agttaacaag
3310

cagtttaatt ttttaagaaat cttaactttt cctgtacatg acacaattga caatccctat
3370

tcctttgtgt ccttgtgttt ggattactcc tgggtatctt tcttctggtc tcttcattta
3430

acctaagtat cattcctcag actttttgct cttaagtcac tggaccgtac ttttgagtaa
3490

tttcaatgca gtaatctcat tttagcttct cagtctgtct ctctgctgtg ctcaactggc
3550

tgcctgttgt cgcttctgca tcttcaagga ctcagtcacc acaaacctac tctatgtttg
3610

tgttccttac ttgggttaatt tcagagccgt tgcaccgttc aaggctttac agttcattcc
3670

tgtatcgtec acctgactat tgggtgtctta agctctgccg attttctctc aacatttcta
3730

tcagtgtttt tcagttttta ttacgatcac caaaggatta cctgtctttt cccatctctc
3790

tgttggctcc tatcaccaga ttgggctttc tagaaacctt cagcctaatt cctgctggca
3850

agtttcatga gcttttttggg gagagtctct gcttgatata caagaccctc ctcttgtgtt
3910

tgccactggt ctgataagag tgttaaaacg ttttcacaaa gtccagagtt gttggccttc
3970

caaacctttg caaacacagt atttgcattg agagccctag gcttctttct catctgggaa
4030

attccatgca tttttgaaat ctgtgaaatt acccctgtcc ccttcctatg gtcaccactg
4090

taactgcaac ctacctctac tgaatcactt attgtactgt atattttatt ttatgaagtg
4150

tcctttatta gaatgtgagc tccttagggg caggaaaaga aactattcat tttggcacct
4210

ctatagcata atgaatagtt tcttttcctg cccctaagga gctcacattc taataaagga
4270

cacttcataa aataaaatat acagtacaat aagtgattca gtagaggtag gttgcagtta
4330

cagtggtgac cataggaagg ggacaggggt aatttcacag atttcaaaaa tg
4382

<210> 6

<211> 464

<212> PRT

<213> Mus sp.

<400> 6

Met Gly Arg Ala Trp Gly Leu Leu Val Gly Leu Leu Gly Val Val Trp
1 5 10 15

Leu Leu Arg Leu Gly His Gly Glu Glu Arg Arg Pro Glu Thr Ala Ala
20 25 30

Gln Arg Cys Phe Cys Gln Val Ser Gly Tyr Leu Asp Asp Cys Thr Cys
35 40 45

Asp Val Glu Thr Ile Asp Lys Phe Asn Asn Tyr Arg Leu Phe Pro Arg
50 55 60

Leu Gln Lys Leu Leu Glu Ser Asp Tyr Phe Arg Tyr Tyr Lys Val Asn
65 70 75 80

Leu Lys Lys Pro Cys Pro Phe Trp Asn Asp Ile Asn Gln Cys Gly Arg
85 90 95

Arg Asp Cys Ala Val Lys Pro Cys His Ser Asp Glu Val Pro Asp Gly
100 105 110

Ile Lys Ser Ala Ser Tyr Lys Tyr Ser Glu Glu Ala Asn Arg Ile Glu
115 120 125

Glu Cys Glu Gln Ala Glu Arg Leu Gly Ala Val Asp Glu Ser Leu Ser
130 135 140

Glu Glu Thr Gln Lys Ala Val Leu Gln Trp Thr Lys His Asp Asp Ser
145 150 155 160

Ser Asp Ser Phe Cys Glu Ile Asp Asp Ile Gln Ser Pro Asp Ala Glu
165 170 175

Tyr Val Asp Leu Leu Leu Asn Pro Glu Arg Tyr Thr Gly Tyr Lys Gly

180					185					190					
Pro	Asp	Ala	Trp	Arg	Ile	Trp	Ser	Val	Ile	Tyr	Glu	Glu	Asn	Cys	Phe
		195					200					205			
Lys	Pro	Gln	Thr	Ile	Gln	Arg	Pro	Leu	Ala	Ser	Gly	Arg	Gly	Lys	Ser
	210					215					220				
Lys	Glu	Asn	Thr	Phe	Tyr	Asn	Trp	Leu	Glu	Gly	Leu	Cys	Val	Glu	Lys
225					230					235					240
Arg	Ala	Phe	Tyr	Arg	Leu	Ile	Ser	Gly	Leu	His	Ala	Ser	Ile	Asn	Val
				245					250					255	
His	Leu	Ser	Ala	Arg	Tyr	Leu	Leu	Gln	Asp	Thr	Trp	Leu	Glu	Lys	Lys
			260					265					270		
Trp	Gly	His	Asn	Val	Thr	Glu	Phe	Gln	Gln	Arg	Phe	Asp	Gly	Ile	Leu
		275					280					285			
Thr	Glu	Gly	Glu	Gly	Pro	Arg	Arg	Leu	Arg	Asn	Leu	Tyr	Phe	Leu	Tyr
	290					295					300				
Leu	Ile	Glu	Leu	Arg	Ala	Leu	Ser	Lys	Val	Leu	Pro	Phe	Phe	Glu	Arg
305					310					315					320
Pro	Asp	Phe	Gln	Leu	Phe	Thr	Gly	Asn	Lys	Val	Gln	Asp	Ala	Glu	Asn
				325					330					335	
Lys	Ala	Leu	Leu	Leu	Glu	Ile	Leu	His	Glu	Ile	Lys	Ser	Phe	Pro	Leu
			340					345					350		
His	Phe	Asp	Glu	Asn	Ser	Phe	Phe	Ala	Gly	Asp	Lys	Asn	Glu	Ala	His
		355					360					365			
Lys	Leu	Lys	Glu	Asp	Phe	Arg	Leu	His	Phe	Arg	Asn	Ile	Ser	Arg	Ile
	370					375					380				
Met	Asp	Cys	Val	Gly	Cys	Phe	Lys	Cys	Arg	Leu	Trp	Gly	Lys	Leu	Gln
385					390					395					400
Thr	Gln	Gly	Leu	Gly	Thr	Ala	Leu	Lys	Ile	Leu	Phe	Ser	Glu	Lys	Leu
				405					410					415	
Ile	Ala	Asn	Met	Pro	Glu	Ser	Gly	Pro	Ser	Tyr	Glu	Phe	Gln	Leu	Thr
			420					425					430		
Arg	Gln	Glu	Ile	Val	Ser	Leu	Phe	Asn	Ala	Phe	Gly	Arg	Ile	Ser	Thr
		435					440					445			
Ser	Val	Arg	Glu	Leu	Glu	Asn	Phe	Arg	His	Leu	Leu	Gln	Asn	Val	His
	450					455					460				

<210> 7
 <211> 2080
 <212> DNA
 <213> Mus sp.

<220>
 <221> CDS
 <222> (46)..(648)

<400> 7
 gtcgacccac gcgtccggag aagactgcaa ctgctcctgg cagac atg aag ccg tac 57
 Met Lys Pro Tyr
 1

ttc tgc cat gtc ttt gtc ttc tgc ttc cta atc aga ctt tta aca gga 105
 Phe Cys His Val Phe Val Phe Cys Phe Leu Ile Arg Leu Leu Thr Gly
 5 10 15 20

gaa atc aat ggc tcg gcc gat cat agg atg ttt tca ttt cac aat gga 153
 Glu Ile Asn Gly Ser Ala Asp His Arg Met Phe Ser Phe His Asn Gly
 25 30 35

ggt gta cag att tct tgt aaa tac cct gag act gtc cag cag tta aaa 201
 Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val Gln Gln Leu Lys
 40 45 50

atg cga ttg ttc aga gag aga gaa gtc ctc tgc gaa ctc acc aag acc 249
 Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu Leu Thr Lys Thr
 55 60 65

aag gga agc gga aat gcg gtg tcc atc aag aat cca atg ctc tgt cta 297
 Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro Met Leu Cys Leu
 70 75 80

tat cat ctg tca aac aac agc gtc tct ttt ttc cta aac aac cca gac 345
 Tyr His Leu Ser Asn Asn Ser Val Ser Phe Phe Leu Asn Asn Pro Asp
 85 90 95 100

agc tcc cag gga agc tat tac ttc tgc agc ctg tcc att ttt gac cca 393
 Ser Ser Gln Gly Ser Tyr Tyr Phe Cys Ser Leu Ser Ile Phe Asp Pro
 105 110 115

cct cct ttt caa gaa agg aac ctt agt gga gga tat ttg cat att tat 441
 Pro Pro Phe Gln Glu Arg Asn Leu Ser Gly Gly Tyr Leu His Ile Tyr
 120 125 130

gaa tcc cag ctc tgc tgc cag ctg aag ctc tgg cta ccc gta ggg tgt 489
 Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu Pro Val Gly Cys
 135 140 145

gca gct ttc gtt gtg gta ctc ctt ttt gga tgc ata ctt atc atc tgg 537
 Ala Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile Leu Ile Ile Trp
 150 155 160

0989545 "1.12001

```

ttt tca aaa aag aaa tac gga tcc agt gtg cat gac cct aat agt gaa 585
Phe Ser Lys Lys Lys Tyr Gly Ser Ser Val His Asp Pro Asn Ser Glu
165 170 175 180

tac atg ttc atg gcg gca gtc aac aca aac aaa aag tct aga ctt gca 633
Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys Ser Arg Leu Ala
185 190 195

ggt gtg acc tca taa gctggaacac ccggacccac agaggaaacg catggactag 688
Gly Val Thr Ser
200

ttccccctgaa acttgaatgg agaaattctt ctatttttctg gaccacaggg cacctgactt 748

gatttaacta cagacaacat tctgctggtg ttttgtttgt ctggatcagt gactatcagt 808

cattcagaat ttcagcagac tgccctgggt ttgctgagtc cttttaagat gaaccccttc 868

ttaaggaaga ccagttcat atatattcaa caaacagacc tctactgggat agaatgcccc 928

tctctccgtg cctgattcta gctatgcact ggccaggaaa acaaacatat ctccagcatt 988

tttttacaaa aaatgccaaag ggtatgaatc tgtaaagcac acaggcagcc aatggccacc
1048

atctgtcctc atttttcaga ttccattttc tttccatgga gatcagcatt ctttctagaa
1108

tcagacagta gagggagatg cttcacaaca gaagcgcttg tgtttctgcg attttgatgt
1168

atatacttta tcgaactcat gcattagaac caacatgctc tttccaatt cctagactct
1228

agctgatcac tgcttcaggg cttagatgcc tgctcttgcc ttcaaatttc cccttaaaga
1288

tatgtccaca tgtctacttg gcagcctgct gccactccaa ataggaagct cagcctacat
1348

tccctcccac cctgttgct caaaaaaaaaa aattagtaga tatgatgttc ccatattctc
1408

cctgccaaag taattttttc cagaaaagac atctaaattc agttaatatg gtttactatg
1468

ttgatattag tggtagtaaa catttctcag aaacaaaagc aaattaattt tgctgtggtg
1528

ttttctacta ttatctgtgt ttccatggtg ctattaatca caagcttagc tatttttgta
1588

gatcatatta aagttgcaag caaggaaagc aaccctctgt taatgggcaa acattctcct
1648

```

ggggtagaat gaattatcta tttagcctga aagctgcggt ttctgggtgg tggctgccag
1708

actacagcca cactttgctc tctctgagtt tgacaggttg aagtagtccc cctggagcag
1768

cactccaggc tacgctggag tcccagagtt gggagatgcc tgggacaagc tgctgctttg
1828

gtctctggga tctgggaagt acagtagggc caagacagaa ttccctctcc tagaaactat
1888

gcagcctgga agtcagccct agcactttaa gatagccttc tttagaatat gagttagttg
1948

gaaggattct gaagtgtaaa gagcatatga ctgctctgag ctggaccatt ttctctactt
2008

tctgtctgt atgcctaaga cttctggagc agccaatgtg tatgcaacat aaaaaaaaaa
2068

aaaaaaaaaa aa
2080

<210> 8
<211> 200
<212> PRT
<213> Mus sp.

<400> 8

Met	Lys	Pro	Tyr	Phe	Cys	His	Val	Phe	Val	Phe	Cys	Phe	Leu	Ile	Arg
1				5				10						15	

Leu	Leu	Thr	Gly	Glu	Ile	Asn	Gly	Ser	Ala	Asp	His	Arg	Met	Phe	Ser
			20					25					30		

Phe	His	Asn	Gly	Gly	Val	Gln	Ile	Ser	Cys	Lys	Tyr	Pro	Glu	Thr	Val
		35					40					45			

Gln	Gln	Leu	Lys	Met	Arg	Leu	Phe	Arg	Glu	Arg	Glu	Val	Leu	Cys	Glu
	50					55					60				

Leu	Thr	Lys	Thr	Lys	Gly	Ser	Gly	Asn	Ala	Val	Ser	Ile	Lys	Asn	Pro
65					70					75					80

Met	Leu	Cys	Leu	Tyr	His	Leu	Ser	Asn	Asn	Ser	Val	Ser	Phe	Phe	Leu
				85					90					95	

Asn	Asn	Pro	Asp	Ser	Ser	Gln	Gly	Ser	Tyr	Tyr	Phe	Cys	Ser	Leu	Ser
			100					105					110		

Ile	Phe	Asp	Pro	Pro	Pro	Phe	Gln	Glu	Arg	Asn	Leu	Ser	Gly	Gly	Tyr
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Gly 70	Ser	Gly	Asn	Ala	Val 75	Ser	Ile	Lys	Asn	Pro 80	Met	Leu	Cys	Leu	Tyr 85		
cat	ctg	tca	aac	aac	agc	gtc	tct	ttt	ttc	cta	aac	aac	cca	gac	agc	342	
His	Leu	Ser	Asn	Asn	Ser	Val	Ser	Phe	Phe	Leu	Asn	Asn	Pro	Asp	Ser		
				90					95					100			
tcc	cag	gga	agc	tat	tac	ttc	tgc	agc	ctg	tcc	att	ttt	gac	cca	cct	390	
Ser	Gln	Gly	Ser	Tyr	Tyr	Phe	Cys	Ser	Leu	Ser	Ile	Phe	Asp	Pro	Pro		
			105					110					115				
cct	ttt	caa	gaa	agg	aac	ctt	agt	gga	gga	tat	ttg	cat	att	tat	gaa	438	
Pro	Phe	Gln	Glu	Arg	Asn	Leu	Ser	Gly	Gly	Tyr	Leu	His	Ile	Tyr	Glu		
		120					125					130					
tcc	cag	ctc	tgc	tgc	cag	ctg	aag	ctc	tgg	cta	ccc	gta	ggg	tgt	gca	486	
Ser	Gln	Leu	Cys	Cys	Gln	Leu	Lys	Leu	Trp	Leu	Pro	Val	Gly	Cys	Ala		
	135					140					145						
gct	ttc	gtt	gtg	gta	ctc	ctt	ttt	gga	tgc	ata	ctt	atc	atc	tgg	ttt	534	
Ala	Phe	Val	Val	Val		Leu	Phe	Gly	Cys	Ile	Leu	Ile	Ile	Trp	Phe		
150					155				160						165		
tca	aaa	aag	aaa	tac	gga	tcc	agt	gtg	cat	gac	cct	aat	agt	gaa	tac	582	
Ser	Lys	Lys	Lys	Tyr	Gly	Ser	Ser	Val	His	Asp	Pro	Asn	Ser	Glu	Tyr		
				170					175					180			
atg	ttc	atg	gcg	gca	gtc	aac	aca	aac	aaa	aag	tct	aga	ctt	gca	ggt	630	
Met	Phe	Met		Ala	Ala	Val	Asn	Thr	Asn	Lys	Lys	Ser	Arg	Leu	Ala		
			185					190					195				
gtg	acc	tca	taa	gctggaacac				ccggacccac				agaggaaacg				682	
Val	Thr	Ser		200								catggactag					
ttccccctgaa			acttgaatgg			agaaattctt			ctatttttctg			gaccacaggg			cacctgactt		742
gatttaacta			cagacaacat			tctgctggtg			ttttgtttgt			ctggatcagt			gactatcagt		802
cattcagaat			ttcagcagac			tgccctgggt			ttgctgagtc			cttttaagat			gaacccttc		862
ttaaggaaga			cccagctcat			atatattcaa			caaacagacc			tactgggat			agaatgcccc		922
tctctccgtg			cctgattcta			gctatgcact			ggccaggaaa			acaaacatat			ctccagcatt		982
tttttacaaa			aaatgccaaag			ggtatgaatc			tgtaaagcac			acaggcagcc					

atatacttta tcgaactcat gcattagaac caacatgctc tcttccaatt cctagactct
1222

agctgatcac tgcttcaggg cttagatgcc tgctcttgcc ttcaaaattt ccccttaaag
1282

atatgtccac atgtctactt ggcagcctgc tgccactcca aataggaagc tcagcctaca
1342

ttccctccca cccctgttgc tcaaaaaaaaa aaattagtag atatgatgtt cccatattct
1402

ccctgccaaa gtaatttttt ccagaaaaga catctaaatt cagttaatat ggtttactat
1462

gttgatatta gtggtagtaa acattttctca gaaacaaaag caaattaatt ttgctgtggg
1522

gttttctact attatctgtg tttccatggg gctattaatc acaagcttag ctatttttgt
1582

agatcatatt aaagttgcaa gcaaggaaaag caaccctctg ttaatgggca aacattctcc
1642

tggggtagaa tgaattatct atttagcctg aaagctgcgg tttctgggtg gtggctgcc
1702

gactacagcc acactttgct ctctctgagt ttgacagggt gaagtagtcc ccctggagca
1762

gcactccagg ctacgctgga gtcccagagt tgggagatgc ctgggacaag ctgctgcttt
1822

ggtctctggg atctgggaag tacagtaggg ccaagacaga attccctctc ctagaaacta
1882

tgcagcctgg aagtcagccc tagcacttta agatagcctt ctttagaata tgagttagtt
1942

ggaaggattc tgaagtgtaa agagcatatg actgctctga gctggaccat tttctctact
2002

ttcctgtctg tatgcctaag acttctggag cagccaatgt gtatgcaaca taaaaaaca
2062

aaaaacaaaa aaactcacia actttaagta aaatatggct gcatcatagt ttttaagttat
2122

agttgcttac ttacagttta ctttaaaagt gagctgtgca tcagtatata gttattacgt
2182

taagcatgtg taatgctggc tatgtacagt acagtactga acgtgtaatt tgaatcaagt
2242

atggtgttct ctctcttcag atgacccggg cagtctgact ggctttgtta gggcattccc
2302

caagttggac ggtcctttct gtgtgagggg gaaggtgctt tactctgttc cttgaaggat
2362

ccccattccc aacacgaaca cctaacaatg acttcttgaa gaacaaaatt tctgtgaaat
2422

aaaatctggc ttaaagagga gccacttgct aaaagatggt agcaataata caaagtaaag
2482

gctaagcact tgtgtgcagc aatgggctat aaccttgctg tgttttctgg ggggtgaagaa
2542

gtgatgacct tagctaccat atgcaaatta gcccttgctc tccaatgacc tttcgtgcta
2602

cataagatag ttgctccctt tgtctcgttt tccccctttt agactctgaa atattcacia
2662

gcttataaaa gagtcagaag cacaggaaac agcacgctct gtgcctgagt tagtttctgc
2722

gttgacctcc tggccccaca gaatgggtgcc tatttcctat ggaaatgaag actgcactct
2782

tgataacttg acagtcacca atatcagaaa attaacactg atatgtcact accctctagt
2842

ctttgggtctg cattcaagat cttcccctgg cttctaggat gtatgtagga gctgaaagtt
2902

ctgctgggga tgtecccttg tgttcgattg acctgtctcg ggagtgttct tcagtctaga
2962

cagttctctt cagcctgtag cctgggccct tttgcagatc acacaccatt attttgtaga
3022

atgttccttt tgtggggggg cacgctgatg tttcttcatg aatgaaatga ggttactcgt
3082

ctttagcaga aataacacag aagtgggtgt gtgccctata gggcgggtca cattttgggt
3142

tgccaagtaa ctgccagtgt ttgttttcat ctctgtcaa gcttctccat tgtaaaggga
3202

ttctgtcctt gaacagccaa taaatatgct ttgtgagaga aaaaaaaaaa ananaaaaaa
3262

aaaa
3266

<210> 10
 <211> 200
 <212> PRT
 <213> Mus sp.

<400> 10
 Met Lys Pro Tyr Phe Cys His Val Phe Val Phe Cys Phe Leu Ile Arg
 1 5 10 15
 Leu Leu Thr Gly Glu Ile Asn Gly Ser Ala Asp His Arg Met Phe Ser
 20 25 30
 Phe His Asn Gly Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val
 35 40 45
 Gln Gln Leu Lys Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu
 50 55 60
 Leu Thr Lys Thr Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro
 65 70 75 80
 Met Leu Cys Leu Tyr His Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
 85 90 95
 Asn Asn Pro Asp Ser Ser Gln Gly Ser Tyr Tyr Phe Cys Ser Leu Ser
 100 105 110
 Ile Phe Asp Pro Pro Pro Phe Gln Glu Arg Asn Leu Ser Gly Gly Tyr
 115 120 125
 Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu
 130 135 140
 Pro Val Gly Cys Ala Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile
 145 150 155 160
 Leu Ile Ile Trp Phe Ser Lys Lys Lys Tyr Gly Ser Ser Val His Asp
 165 170 175
 Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys
 180 185 190
 Ser Arg Leu Ala Gly Val Thr Ser
 195 200

<210> 11
 <211> 2703
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> (115)..(711)

<400> 11

```

tccggaattc cggggtcgac ccacgcgtcc gcggacgcgt gggcggacgc gtgggcggac 60

gcgtgggcgg acgcgtgggc tgaacgcgag gactgttaac tgtttctggc aaac atg 117
                                         Met
                                         1

aag tca ggc ctc tgg tat ttc ttt ctc ttc tgc ttg cgc att aaa gtt 165
Lys Ser Gly Leu Trp Tyr Phe Phe Leu Phe Cys Leu Arg Ile Lys Val
                    5                      10                      15

tta aca gga gaa atc aat ggt tct gcc aat tat gag atg ttt ata ttt 213
Leu Thr Gly Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met Phe Ile Phe
                    20                      25                      30

cac aac gga ggt gta caa att tta tgc aaa tat cct gac att gtc cag 261
His Asn Gly Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val Gln
                    35                      40                      45

caa ttt aaa atg cag ttg ctg aaa ggg ggg caa ata ctc tgc gat ctc 309
Gln Phe Lys Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp Leu
                    50                      55                      60                      65

act aag aca aaa gga agt gga aac aca gtg tcc att aag agt ctg aaa 357
Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu Lys
                    70                      75                      80

ttc tgc cat tct cag tta tcc aac aac agt gtc tct ttt ttt cta tac 405
Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu Tyr
                    85                      90                      95

aac ttg gac cat tct cat gcc aac tat tac ttc tgc aac cta tca att 453
Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser Ile
                    100                      105                      110

ttt gat cct cct cct ttt aaa gta act ctt aca gga gga tat ttg cat 501
Phe Asp Pro Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu His
                    115                      120                      125

att tat gaa tca caa ctt tgt tgc cag ctg aag ttc tgg tta ccc ata 549
Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro Ile
                    130                      135                      140                      145

gga tgt gca gcc ttt gtt gta gtc tgc att ttg gga tgc ata ctt att 597
Gly Cys Ala Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu Ile
                    150                      155                      160

tgt tgg ctt aca aaa aag tat tca tcc agt gtg cac gac cct aac ggt 645
Cys Trp Leu Thr Lys Lys Tyr Ser Ser Ser Val His Asp Pro Asn Gly
                    165                      170                      175

gaa tac atg ttc atg aga gca gtg aac aca gcc aaa aaa tct aga ctc 693

```

Glu Tyr Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser Arg Leu	
180	185 190

aca gat gtg acc cta taa tatggaactc tggcaccag gcatgaagca 741
 Thr Asp Val Thr Leu
 195

cggtggccag ttttccctcaa cttgaagtgc aagattctct tatttccggg accacggaga 801
 gtctgactta actacatata tcttctgctg gtgttttggt caatctggaa gaatgactgt 861
 atcagtcaat ggggatttta acagactgcc ttggtactgc cgagtcctct caaaacaaac 921
 accctcttgc aaccagcttt ggagaaagcc cagctcctgt gtgctcactg ggagtggaat 981
 ccctgtctcc acatctgctc ctagcagtgc atcagccagt aaaacaaaca catttacaag
 1041

aaaaatgttt taaagatgcc aggggtactg aatctgcaa gcaaatgagc agccaaggac
 1101

cagcatctgt ccgcatttca ctatcatact acctcttctt tctgtaggga tgagaattcc
 1161

tcttttaatc agtgaaggga gatgcttcaa agctggagct attttatttc tgagatgttg
 1221

atgtgaactg tacattagta catactcagt actctccttc aattgctgaa cccagttga
 1281

ccattttacc aagacttttag atgctttctt gtgccctcaa ttttcttttt aaaaatactt
 1341

ctacatgact gcttgacagc ccaacagcca ctctcaatag agagctatgt cttacattct
 1401

ttcctctgct gctcaatagt tttatatatc tatgcatata tatatacaca catatgtata
 1461

taaaattcat aatgaatata tttgcctata ttctccctac aagaatattt ttgctccaga
 1521

aagacatggt cttttctcaa attcagttaa aatgggttac tttgttcaag ttagtggttag
 1581

gaaacattgc ccggaattga aagcaaattt attttattat cctattttct accattatct
 1641

atgttttcat ggtgctatta attacaagtt tagttctttt tgtacgatca tattaataatt
 1701

gaaacaaaa tcattctttaa tgggccagca ttctcatggg gtagagcaga atattcattt
 1761

agcctgaaag ctgcagttac tataggttgc tgtcagacta taccatggt gcctctgggc
1821

ttgacaggtc aaaatgggtcc ccatcagcct ggagcagccc tccagacctg ggtggaattc
1881

caggggttgag agactccct gagccagagg ccactaggta ttcttgctcc cagaggctga
1941

agtcaccctg ggaatcacag tgggtctacct gcattcataa ttccaggatc tgtgaagagc
2001

acatatgtgt cagggcaciaa ttccctctca taaaaaccac acagcctgga aattggccct
2061

ggcccttcaa gatagccttc tttagaatat gatttggtta gaaagattct taaatatgtg
2121

gaatatgatt attcttagct ggaatatatt ctctacttcc tgtctgcatg cccaaggctt
2181

ctgaagcagc caatgtcgat gcaacaacat ttgtaacttt aggtaaactg ggattatgtt
2241

gtagttaaac attttgtaac tgtgtgctta tagtttaciaa gtgagacctg atatgtcatt
2301

atgcatactt atattatctt aagcatgtgt aatgctggat gtgtacagta cagtactgaa
2361

cttgtaattt gaatctagta tgggtgttctg ttttcagctg acttggaciaa cctgactggc
2421

tttgcacagg tgttccctga gttgtttgca ggtttctgtg tgtgggggtg ggtatgggga
2481

ggagaacctt catgggtggc cacctggcct gggtgtccaa gctgtgcctc gacacatcct
2541

catccccagc atgggacacc tcaagatgaa taataattca caaaatttct gtgaaatcaa
2601

atccagtttt aagaggagcc acttatcaaa gagattttta cagtagtaag aaggcaaaga
2661

ataaacattt gatattcagc aactgaaaaa aaaaaaaaaa aa
2703

<210> 12

<211> 198

<212> PRT

<213> Homo sapiens

```

<400> 12
Met Lys Ser Gly Leu Trp Tyr Phe Phe Leu Phe Cys Leu Arg Ile Lys
 1          5          10          15

Val Leu Thr Gly Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met Phe Ile
      20          25          30

Phe His Asn Gly Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val
      35          40          45

Gln Gln Phe Lys Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp
 50          55          60

Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu
 65          70          75          80

Lys Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
      85          90          95

Tyr Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser
      100          105          110

Ile Phe Asp Pro Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu
      115          120          125

His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro
      130          135          140

Ile Gly Cys Ala Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu
 145          150          155          160

Ile Cys Trp Leu Thr Lys Lys Tyr Ser Ser Ser Val His Asp Pro Asn
      165          170          175

Gly Glu Tyr Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser Arg
      180          185          190

Leu Thr Asp Val Thr Leu
      195

```

```

<210> 13
<211> 1795
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (57)..(1502)

```

```

<400> 13
gtcgacccac gcgctccgggc ctcccaagcg tggggcgaca agctgccgga gctgca atg 59
                                         Met
                                         1

```

ggc	cgc	ggc	tgg	gga	ttc	ttg	ttt	ggc	ctc	ctg	ggc	gcc	gtg	tgg	ctg	107
Gly	Arg	Gly	Trp	Gly	Phe	Leu	Phe	Gly	Leu	Leu	Gly	Ala	Val	Trp	Leu	
			5							10				15		
ctc	agc	tcg	ggc	cac	gga	gag	gag	cag	ccc	ccg	gag	aca	gcg	gca	cag	155
Leu	Ser	Ser	Gly	His	Gly	Glu	Glu	Gln	Pro	Pro	Glu	Thr	Ala	Ala	Gln	
			20							25				30		
agg	tgc	ttc	tgc	cag	gtt	agt	ggt	tac	ttg	gat	gat	tgt	acc	tgt	gat	203
Arg	Cys	Phe	Cys	Gln	Val	Ser	Gly	Tyr	Leu	Asp	Asp	Cys	Thr	Cys	Asp	
			35							40				45		
gtt	gaa	acc	att	gat	aga	ttt	aat	aac	tac	agg	ctt	ttc	cca	aga	cta	251
Val	Glu	Thr	Ile	Asp	Arg	Phe	Asn	Asn	Tyr	Arg	Leu	Phe	Pro	Arg	Leu	
			50							55				60		
caa	aaa	ctt	ctt	gaa	agt	gac	tac	ttt	agg	tat	tac	aag	gta	aac	ctg	299
Gln	Lys	Leu	Leu	Glu	Ser	Asp	Tyr	Phe	Arg	Tyr	Tyr	Lys	Val	Asn	Leu	
			65							70				75		
aag	agg	ccg	tgt	cct	ttc	tgg	aat	gac	atc	agc	cag	tgt	gga	aga	agg	347
Lys	Arg	Pro	Cys	Pro	Phe	Trp	Asn	Asp	Ile	Ser	Gln	Cys	Gly	Arg	Arg	
			85							90				95		
gac	tgt	gct	gtc	aaa	cca	tgt	caa	tct	gat	gaa	gtt	cct	gat	gga	att	395
Asp	Cys	Ala	Val	Lys	Pro	Cys	Gln	Ser	Asp	Glu	Val	Pro	Asp	Gly	Ile	
			100							105				110		
aaa	tct	gcg	agc	tac	aag	tat	tct	gaa	gaa	gcc	aat	aat	ctc	att	gaa	443
Lys	Ser	Ala	Ser	Tyr	Lys	Tyr	Ser	Glu	Glu	Ala	Asn	Asn	Leu	Ile	Glu	
			115							120				125		
gaa	tgt	gaa	caa	gct	gaa	cga	ctt	gga	gca	gtg	gat	gaa	tct	ctg	agt	491
Glu	Cys	Glu	Gln	Ala	Glu	Arg	Leu	Gly	Ala	Val	Asp	Glu	Ser	Leu	Ser	
			130							135				140		
gag	gaa	aca	cag	aag	gct	gtt	ctt	cag	tgg	acc	aag	cat	gat	gat	tct	539
Glu	Glu	Thr	Gln	Lys	Ala	Val	Leu	Gln	Trp	Thr	Lys	His	Asp	Asp	Ser	
			145							150				155		
tca	gat	aac	ttc	tgt	gaa	gct	gat	gat	tgg	atc	tgc	tgg	tgg	tca	tct	587
Ser	Asp	Asn	Phe	Cys	Glu	Ala	Asp	Asp	Trp	Ile	Cys	Trp	Trp	Ser	Ser	
			165							170				175		
aag	aag	aaa	gta	ttt	gac	att	cag	tcc	cct	gaa	gct	gaa	tat	gta	gat	635
Lys	Lys	Lys	Val	Phe	Asp	Ile	Gln	Ser	Pro	Glu	Ala	Glu	Tyr	Val	Asp	
			180							185				190		
ttg	ctt	ctt	aat	cct	gag	cgc	tac	act	ggt	tac	aag	gga	cca	gat	gct	683
Leu	Leu	Leu	Asn	Pro	Glu	Arg	Tyr	Thr	Gly	Tyr	Lys	Gly	Pro	Asp	Ala	
			195							200				205		
tgg	aaa	ata	tgg	aat	gtc	atc	tac	gaa	gaa	aac	tgt	ttt	aag	cca	cag	731

Trp Lys Ile Trp Asn Val Ile Tyr Glu Glu Asn Cys Phe Lys Pro Gln	
210 215 220 225	
aca att aaa aga cct tta aat cct ttg gct tct ggt caa ggg aca agt	779
Thr Ile Lys Arg Pro Leu Asn Pro Leu Ala Ser Gly Gln Gly Thr Ser	
230 235 240	
gaa gag aac act ttt tac agt tgg cta gaa ggt ctc tgt gta gaa aaa	827
Glu Glu Asn Thr Phe Tyr Ser Trp Leu Glu Gly Leu Cys Val Glu Lys	
245 250 255	
aga gca ttc tac aga ctt ata tct ggc cta cat gca agc att aat gtg	875
Arg Ala Phe Tyr Arg Leu Ile Ser Gly Leu His Ala Ser Ile Asn Val	
260 265 270	
cat ttg agt gca aga tat ctt tta caa gag acc tgg tta gaa aag aaa	923
His Leu Ser Ala Arg Tyr Leu Leu Gln Glu Thr Trp Leu Glu Lys Lys	
275 280 285	
tgg gga cac aac att aca gaa ttt caa cag cga ttt gat gga att ttg	971
Trp Gly His Asn Ile Thr Glu Phe Gln Gln Arg Phe Asp Gly Ile Leu	
290 295 300 305	
act gaa gga gaa ggt cca aga agg ctt aag aac ttg tat ttt ctc tac	
1019 Thr Glu Gly Glu Gly Pro Arg Arg Leu Lys Asn Leu Tyr Phe Leu Tyr	
310 315 320	
tta ata gaa cta agg gcc tta tcc aaa gtg tta cca ttc ttc gag cgc	
1067 Leu Ile Glu Leu Arg Ala Leu Ser Lys Val Leu Pro Phe Phe Glu Arg	
325 330 335	
cca gat ttt caa ctc ttt act gga aat aaa att cag gat gag gaa aac	
1115 Pro Asp Phe Gln Leu Phe Thr Gly Asn Lys Ile Gln Asp Glu Glu Asn	
340 345 350	
aaa atg tta ctt ctg gaa ata ctt cat gaa atc aag tca ttt cct ttg	
1163 Lys Met Leu Leu Leu Glu Ile Leu His Glu Ile Lys Ser Phe Pro Leu	
355 360 365	
cat ttt gat gag aat tca ttt ttt gct ggg gat aaa aaa gaa gca cac	
1211 His Phe Asp Glu Asn Ser Phe Phe Ala Gly Asp Lys Lys Glu Ala His	
370 375 380 385	
aaa cta aag gag gac ttt cga ctg cat ttt aga aat att tca aga att	
1259 Lys Leu Lys Glu Asp Phe Arg Leu His Phe Arg Asn Ile Ser Arg Ile	
390 395 400	

atg gat tgt gtt ggt tgt ttt aaa tgt cgt ctg tgg gga aag ctt cag
1307
Met Asp Cys Val Gly Cys Phe Lys Cys Arg Leu Trp Gly Lys Leu Gln
405 410 415

act cag ggt ttg ggc act gct ctg aag atc tta ttt tct gag aaa ttg
1355
Thr Gln Gly Leu Gly Thr Ala Leu Lys Ile Leu Phe Ser Glu Lys Leu
420 425 430

ata gca aat atg cca gaa agt gga cct agt tat gaa ttc cat cta acc
1403
Ile Ala Asn Met Pro Glu Ser Gly Pro Ser Tyr Glu Phe His Leu Thr
435 440 445

aga caa gaa ata gta tca tta ttc aac gca ttt gga aga att tct aca
1451
Arg Gln Glu Ile Val Ser Leu Phe Asn Ala Phe Gly Arg Ile Ser Thr
450 455 460 465

agt gtg aaa gaa tta gaa aac ttc agg aac ttg tta cag aat att cat
1499
Ser Val Lys Glu Leu Glu Asn Phe Arg Asn Leu Leu Gln Asn Ile His
470 475 480

taa agaaaacaag ctgatatgtg cctgtttctg gacaatggag gcgaaagagt
1552

ggaatttcat tcaaaggcat aatagcaatg acagtcttaa gccaaacatt ttatataaag
1612

ttgcttttgt aaaggagaat tatattgttt taagtaaaca cattttttaa aattgtgtta
1672

agtctatgta taatactact gtgagtaaaa gtaatacttt aataatgtgg tacaaatttt
1732

aaagtttaat attgaataaaa aggaggatta tcaaattcaa aaaaaaaaaa aaagggcggc
1792

cgc
1795

<210> 14
<211> 481
<212> PRT
<213> Homo sapiens

<400> 14
Met Gly Arg Gly Trp Gly Phe Leu Phe Gly Leu Leu Gly Ala Val Trp
1 5 10 15

Leu	Leu	Ser	Ser	Gly	His	Gly	Glu	Glu	Gln	Pro	Pro	Glu	Thr	Ala	Ala		
			20					25					30				
Gln	Arg	Cys	Phe	Cys	Gln	Val	Ser	Gly	Tyr	Leu	Asp	Asp	Cys	Thr	Cys		
		35					40					45					
Asp	Val	Glu	Thr	Ile	Asp	Arg	Phe	Asn	Asn	Tyr	Arg	Leu	Phe	Pro	Arg		
	50					55					60						
Leu	Gln	Lys	Leu	Leu	Glu	Ser	Asp	Tyr	Phe	Arg	Tyr	Tyr	Lys	Val	Asn		
	65				70					75					80		
Leu	Lys	Arg	Pro	Cys	Pro	Phe	Trp	Asn	Asp	Ile	Ser	Gln	Cys	Gly	Arg		
				85					90					95			
Arg	Asp	Cys	Ala	Val	Lys	Pro	Cys	Gln	Ser	Asp	Glu	Val	Pro	Asp	Gly		
			100					105					110				
Ile	Lys	Ser	Ala	Ser	Tyr	Lys	Tyr	Ser	Glu	Glu	Ala	Asn	Asn	Leu	Ile		
		115					120						125				
Glu	Glu	Cys	Glu	Gln	Ala	Glu	Arg	Leu	Gly	Ala	Val	Asp	Glu	Ser	Leu		
	130					135					140						
Ser	Glu	Glu	Thr	Gln	Lys	Ala	Val	Leu	Gln	Trp	Thr	Lys	His	Asp	Asp		
	145				150					155				160			
Ser	Ser	Asp	Asn	Phe	Cys	Glu	Ala	Asp	Asp	Trp	Ile	Cys	Trp	Trp	Ser		
				165					170					175			
Ser	Lys	Lys	Lys	Val	Phe	Asp	Ile	Gln	Ser	Pro	Glu	Ala	Glu	Tyr	Val		
			180					185					190				
Asp	Leu	Leu	Leu	Asn	Pro	Glu	Arg	Tyr	Thr	Gly	Tyr	Lys	Gly	Pro	Asp		
	195						200					205					
Ala	Trp	Lys	Ile	Trp	Asn	Val	Ile	Tyr	Glu	Glu	Asn	Cys	Phe	Lys	Pro		
	210					215					220						
Gln	Thr	Ile	Lys	Arg	Pro	Leu	Asn	Pro	Leu	Ala	Ser	Gly	Gln	Gly	Thr		
	225				230					235					240		
Ser	Glu	Glu	Asn	Thr	Phe	Tyr	Ser	Trp	Leu	Glu	Gly	Leu	Cys	Val	Glu		
				245					250					255			
Lys	Arg	Ala	Phe	Tyr	Arg	Leu	Ile	Ser	Gly	Leu	His	Ala	Ser	Ile	Asn		
			260					265					270				
Val	His	Leu	Ser	Ala	Arg	Tyr	Leu	Leu	Gln	Glu	Thr	Trp	Leu	Glu	Lys		
		275					280					285					
Lys	Trp	Gly	His	Asn	Ile	Thr	Glu	Phe	Gln	Gln	Arg	Phe	Asp	Gly	Ile		
	290					295					300						

Leu Thr Glu Gly Glu Gly Pro Arg Arg Leu Lys Asn Leu Tyr Phe Leu
 305 310 315 320

Tyr Leu Ile Glu Leu Arg Ala Leu Ser Lys Val Leu Pro Phe Phe Glu
 325 330 335

Arg Pro Asp Phe Gln Leu Phe Thr Gly Asn Lys Ile Gln Asp Glu Glu
 340 345 350

Asn Lys Met Leu Leu Leu Glu Ile Leu His Glu Ile Lys Ser Phe Pro
 355 360 365

Leu His Phe Asp Glu Asn Ser Phe Phe Ala Gly Asp Lys Lys Glu Ala
 370 375 380

His Lys Leu Lys Glu Asp Phe Arg Leu His Phe Arg Asn Ile Ser Arg
 385 390 395 400

Ile Met Asp Cys Val Gly Cys Phe Lys Cys Arg Leu Trp Gly Lys Leu
 405 410 415

Gln Thr Gln Gly Leu Gly Thr Ala Leu Lys Ile Leu Phe Ser Glu Lys
 420 425 430

Leu Ile Ala Asn Met Pro Glu Ser Gly Pro Ser Tyr Glu Phe His Leu
 435 440 445

Thr Arg Gln Glu Ile Val Ser Leu Phe Asn Ala Phe Gly Arg Ile Ser
 450 455 460

Thr Ser Val Lys Glu Leu Glu Asn Phe Arg Asn Leu Leu Gln Asn Ile
 465 470 475 480

His

<210> 15
 <211> 3868
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (325)..(1479)

<400> 15
 gcggcgcgtc gcgcgcagcc ccgcacctcc gccctgcct ctgcctcctg ggccatgccc 60
 tgctgtttac atgccggtga ggtccccggc cgctccgaac cctccgagc cccggctccc 120
 cgaggggtgaa gcccgccggc ccgcgaactg gactggtgga tctctcagac ctggggccccc 180
 ggactccgat ctccgcgcgc tccgccacca tcagggcggg atccggctct ggtgttttga 240

```

ggaggggggtg tgggtgtaggg aaaggaatcc cgccccctctc caccttttttt cgccttcggg 300

gcttcagact cagggaactc gctc atg gct ttc ttg atg aag aag aag aaa 351
                Met Ala Phe Leu Met Lys Lys Lys Lys
                1                    5

ttc aaa ttc caa act act ttc acc ctg gag gag ctg act gcg gtt ccc 399
Phe Lys Phe Gln Thr Thr Phe Thr Leu Glu Glu Leu Thr Ala Val Pro
10                    15                    20                    25

ttc gtg aac ggg gtc ctc ttc tgc aag gtc cgg ctg ctg gat gga ggg 447
Phe Val Asn Gly Val Leu Phe Cys Lys Val Arg Leu Leu Asp Gly Gly
30                    35                    40

gat ttt gtc agc ttg tcg tca agg gag gag gta cag gag aac tgt gtg 495
Asp Phe Val Ser Leu Ser Ser Arg Glu Glu Val Gln Glu Asn Cys Val
45                    50                    55

cgg tgg cga aag agg ttc acc ttc gtg tgt aag atg agt gct aac ccg 543
Arg Trp Arg Lys Arg Phe Thr Phe Val Cys Lys Met Ser Ala Asn Pro
60                    65                    70

gcc acc ggc ctg ctg gac ccc tgt gtc ttc cgt gtg tct gtg cgc aag 591
Ala Thr Gly Leu Leu Asp Pro Cys Val Phe Arg Val Ser Val Arg Lys
75                    80                    85

gag ctg aaa ggc ggg aag gct tat tcc aag ctg ggc ttc gct gac ttg 639
Glu Leu Lys Gly Gly Lys Ala Tyr Ser Lys Leu Gly Phe Ala Asp Leu
90                    95                    100                    105

aac ctg gcc gag ttt gcg ggc tcg ggc tcc acg gtg cgc tgc tgc ctg 687
Asn Leu Ala Glu Phe Ala Gly Ser Gly Ser Thr Val Arg Cys Cys Leu
110                    115                    120

ctc gag gga tat gac acg aag aac act cgc cag gac aac tcc atc ctt 735
Leu Glu Gly Tyr Asp Thr Lys Asn Thr Arg Gln Asp Asn Ser Ile Leu
125                    130                    135

aag gtc acc att ggt atg ttc ctg ctc tct gga gat ccc tgc ttc aag 783
Lys Val Thr Ile Gly Met Phe Leu Leu Ser Gly Asp Pro Cys Phe Lys
140                    145                    150

acg cca cca tcg act gcc aag tcc atc tcc atc cca ggc cag gat tcc 831
Thr Pro Pro Ser Thr Ala Lys Ser Ile Ser Ile Pro Gly Gln Asp Ser
155                    160                    165

tcc ctg cag ctg acg tgt aag ggt ggt ggg acc agc agt ggg ggc agc 879
Ser Leu Gln Leu Thr Cys Lys Gly Gly Gly Thr Ser Ser Gly Gly Ser
170                    175                    180                    185

agc acc aac tcc ctg act ggg tcc cgg ccc ccc aag gct cgg ccc act 927
Ser Thr Asn Ser Leu Thr Gly Ser Arg Pro Pro Lys Ala Arg Pro Thr
190                    195                    200

```

att ctc agc tca ggg ctg cca gag gaa ccc gac cag aac ctg tcc agc 975
Ile Leu Ser Ser Gly Leu Pro Glu Glu Pro Asp Gln Asn Leu Ser Ser
205 210 215

cct gag gag gtg ttc cac tct ggc cac tcc cgc aac tcc agc tat gcc
1023
Pro Glu Glu Val Phe His Ser Gly His Ser Arg Asn Ser Ser Tyr Ala
220 225 230

agc cag cag tcc aag atc tcc ggc tac agc aca gag cac tcg cgc tcc
1071
Ser Gln Gln Ser Lys Ile Ser Gly Tyr Ser Thr Glu His Ser Arg Ser
235 240 245

tcc agc ctc tca gac ctg acg cac cgc cgc aac acg tcc acc agc agc
1119
Ser Ser Leu Ser Asp Leu Thr His Arg Arg Asn Thr Ser Thr Ser Ser
250 255 260 265

agc gcc tct ggg ggc ctt ggc atg acc gtg gag ggc cct gag ggc agt
1167
Ser Ala Ser Gly Gly Leu Gly Met Thr Val Glu Gly Pro Glu Gly Ser
270 275 280

gag cgg gag cac cgg ccc ccg gag aag ccg ccg cgg cca ccc cgg ccc
1215
Glu Arg Glu His Arg Pro Pro Glu Lys Pro Pro Arg Pro Pro Arg Pro
285 290 295

ctg cat ctg tcc gat cgc tct ttc agg cgg aag aag gac tcg gtg gag
1263
Leu His Leu Ser Asp Arg Ser Phe Arg Arg Lys Lys Asp Ser Val Glu
300 305 310

agc cac ccg acc tgg gtg gac gac acg cgg atc gat gcg gat gcc atc
1311
Ser His Pro Thr Trp Val Asp Asp Thr Arg Ile Asp Ala Asp Ala Ile
315 320 325

gtg gag aag atc gtg cag agc cag gac ttc aca gat ggc agc aac acc
1359
Val Glu Lys Ile Val Gln Ser Gln Asp Phe Thr Asp Gly Ser Asn Thr
330 335 340 345

gag gac agc aac ctc cgg ctg ttc gtg agc cgc gat ggc tct gcc acg
1407
Glu Asp Ser Asn Leu Arg Leu Phe Val Ser Arg Asp Gly Ser Ala Thr
350 355 360

ctg agc ggc atc cag ctt gcc acc agg gtc tct tct ggg gtc tac gag
1455
Leu Ser Gly Ile Gln Leu Ala Thr Arg Val Ser Ser Gly Val Tyr Glu
365 370 375

gcggatgcca gagaggcagg tgggctgtgg ctggactggg ccggagctgg cttccttacc
2529

agaaaagcct cagccttcct ctggaagcat cccccgttct gggcaagggg gaagggctcc
2589

tttaaggggt gtgctttccc agtgggggagc agtctggccc tgccccctac taaagcctct
2649

gctctcagca ctttccccca agtccttgta acttgcttga aggtgggttc tggctgccag
2709

ccagtccctg gacaaactct cctgcccctt ttaaatttca ctcattttgt ataaaccag
2769

caggctgggtg ttacttagc cctgtagctt ttttcatttt ttctttccgt ctttcttctt
2829

gagttcacgg ttcaatattg cctcctcgcc ctggtgaggg gaggtgctgc ttttctgccc
2889

cacctgccgg ctggttccag cagcgctggg gccagctgg ggggccggga tgggggcttc
2949

tctctctggg aggggtgcag gtgccctccc caggctggga gggttccttc cctagctccc
3009

catctgcccc cgctggtgag agttgggctt ctggtcttg gaactccctg gcattgggaa
3069

cagagcattt ccagcatttg ttgttgttgt ttactcacc taacccttag aaaatgaatg
3129

ttagaagggt cctgccgagg cgggacagag tgtttgctcg cgctggagaa ggctctgctc
3189

agccctgaga gtcccttcct gccccaccga tactggcact ttaaaaagga agctgaccgc
3249

acagtgtcca gacgaattgg cccccagaag atggggagtt ctgtcctgcc cttctgtgtc
3309

tgcgtgacct caccagcct aggagggagg tgcattcagg gtagatttgc ctctcattca
3369

aagttctggg gctttgggcg gaaaacagcc agctttggcg ctggtgggga gactcctcca
3429

gaccaggaac ccagaagga gacagagcct gccacatcct cccacgccag gccctgggcc
3489

agggtgattg gactgagaat ttggccacaa ccaaattgat gctggctgga accagaggcc
3549

agaaagcctg gccttgcccc catgtgggag ccctgtcctc agccctcttg tcccccttgag
3609

ctcagtgaat tcccaccagg tgcccacagc tcctggactt caaattctat atattgagag
3669

agttggagag tatatcagag atatTTTTtg aaaggagttg gtctatgcaa tgtcagtttg
3729

gaatcttctt gaaagtttaa tgTTTTtatt aggagattta aagaaaataa aggtctacaa
3789

tatcaaaaaa aaaacccacg cgtccgccca cgcgtccgcc cacgcgtccg cccacgcgtc
3849

cgcgagacgc tgggtcgac
3868

<210> 16

<211> 384

<212> PRT

<213> Homo sapiens

<400> 16

Met	Ala	Phe	Leu	Met	Lys	Lys	Lys	Lys	Phe	Lys	Phe	Gln	Thr	Thr	Phe
1				5					10					15	

Thr	Leu	Glu	Glu	Leu	Thr	Ala	Val	Pro	Phe	Val	Asn	Gly	Val	Leu	Phe
			20					25					30		

Cys	Lys	Val	Arg	Leu	Leu	Asp	Gly	Gly	Asp	Phe	Val	Ser	Leu	Ser	Ser
		35					40					45			

Arg	Glu	Glu	Val	Gln	Glu	Asn	Cys	Val	Arg	Trp	Arg	Lys	Arg	Phe	Thr
	50					55					60				

Phe	Val	Cys	Lys	Met	Ser	Ala	Asn	Pro	Ala	Thr	Gly	Leu	Leu	Asp	Pro
65					70					75					80

Cys	Val	Phe	Arg	Val	Ser	Val	Arg	Lys	Glu	Leu	Lys	Gly	Gly	Lys	Ala
				85					90					95	

Tyr	Ser	Lys	Leu	Gly	Phe	Ala	Asp	Leu	Asn	Leu	Ala	Glu	Phe	Ala	Gly
			100					105					110		

Ser	Gly	Ser	Thr	Val	Arg	Cys	Cys	Leu	Leu	Glu	Gly	Tyr	Asp	Thr	Lys
		115					120					125			

Asn	Thr	Arg	Gln	Asp	Asn	Ser	Ile	Leu	Lys	Val	Thr	Ile	Gly	Met	Phe
	130					135					140				

Leu	Leu	Ser	Gly	Asp	Pro	Cys	Phe	Lys	Thr	Pro	Pro	Ser	Thr	Ala	Lys
145					150					155					160

Ser Ile Ser Ile Pro Gly Gln Asp Ser Ser Leu Gln Leu Thr Cys Lys
165 170 175

Gly Gly Gly Thr Ser Ser Gly Gly Ser Ser Thr Asn Ser Leu Thr Gly
180 185 190

Ser Arg Pro Pro Lys Ala Arg Pro Thr Ile Leu Ser Ser Gly Leu Pro
195 200 205

Glu Glu Pro Asp Gln Asn Leu Ser Ser Pro Glu Glu Val Phe His Ser
210 215 220

Gly His Ser Arg Asn Ser Ser Tyr Ala Ser Gln Gln Ser Lys Ile Ser
225 230 235 240

Gly Tyr Ser Thr Glu His Ser Arg Ser Ser Ser Leu Ser Asp Leu Thr
245 250 255

His Arg Arg Asn Thr Ser Thr Ser Ser Ser Ala Ser Gly Gly Leu Gly
260 265 270

Met Thr Val Glu Gly Pro Glu Gly Ser Glu Arg Glu His Arg Pro Pro
275 280 285

Glu Lys Pro Pro Arg Pro Pro Arg Pro Leu His Leu Ser Asp Arg Ser
290 295 300

Phe Arg Arg Lys Lys Asp Ser Val Glu Ser His Pro Thr Trp Val Asp
305 310 315 320

Asp Thr Arg Ile Asp Ala Asp Ala Ile Val Glu Lys Ile Val Gln Ser
325 330 335

Gln Asp Phe Thr Asp Gly Ser Asn Thr Glu Asp Ser Asn Leu Arg Leu
340 345 350

Phe Val Ser Arg Asp Gly Ser Ala Thr Leu Ser Gly Ile Gln Leu Ala
355 360 365

Thr Arg Val Ser Ser Gly Val Tyr Glu Pro Val Val Ile Glu Ser His
370 375 380

<210> 17
<211> 442
<212> PRT
<213> Trypanosoma brucei

<400> 17
Met Leu Lys Met Arg Leu Leu Ile Val Val Pro Val Leu Leu Gly Leu
1 5 10 15
Val Trp Gln Ile Leu Leu Arg Ala Glu Leu Asp Gly Val Ser Phe Phe

				20						25						30			
Gly	Met	Tyr	Ile	Ser	Ala	Asn	Asn	Ser	Gly	Ala	Gly	Ser	Tyr	Val	Arg				
		35					40					45							
Thr	Lys	Lys	Gly	Asn	Ala	Leu	Lys	Glu	Gly	Phe	Cys	Ser	Leu	Thr	Met				
	50					55					60								
Asp	Glu	Val	Ser	Gln	Asn	Thr	Glu	Gly	Ile	Thr	Gly	Leu	Leu	Asn	Asn				
	65				70					75					80				
Ile	Thr	Ser	His	Pro	Tyr	Phe	Arg	Tyr	Phe	Lys	Val	Asn	Leu	Asp	Arg				
				85					90					95					
Glu	Cys	Arg	Tyr	Trp	Val	Ala	Glu	Ala	Ser	Cys	Thr	Cys	Asp	Ser	Asn				
			100					105					110						
Gly	Cys	Gln	Ile	Cys	Thr	Cys	Asp	Asp	Ser	Gly	Ile	Pro	Glu	Thr	Leu				
		115					120					125							
Lys	Tyr	Pro	Tyr	Asp	Met	Ser	Asp	Val	Ser	Ala	Val	Glu	Arg	Arg	Thr				
	130					135					140								
Ala	Pro	Asp	Lys	His	Ala	Ala	Lys	Gly	Phe	Glu	Asp	Glu	Ile	Lys	Pro				
	145				150					155					160				
Ile	Asp	Pro	Asp	Arg	Asp	Ala	Thr	Tyr	Val	Asp	Leu	Leu	Gln	Asn	Pro				
				165					170					175					
Glu	Ala	Asn	Thr	Gly	Tyr	Ser	Gly	Pro	Lys	Ala	Ala	Arg	Val	Trp	Gln				
			180					185					190						
Ala	Val	Tyr	Asp	Asn	Cys	Asn	Ile	Asp	Gly	Leu	Pro	Ser	Asn	Asp	Thr				
		195					200					205							
Ala	Gly	Val	Glu	Asn	Arg	Glu	Lys	Ala	Leu	Leu	Arg	Gln	Leu	Leu	Ser				
	210					215					220								
Gly	Leu	His	Thr	Ser	Ile	Thr	Met	His	Val	Ala	Ala	Phe	Phe	Tyr	Asn				
	225				230				235						240				
Asp	Thr	Lys	Gly	Asp	Ser	Pro	Leu	Arg	Ser	Leu	Gly	Val	Leu	Asn	Asn				
				245					250					255					
Pro	Asn	Ile	Ser	Phe	Tyr	Pro	Asn	Cys	Gly	Met	Phe	Arg	Arg	Ile	Val				
			260					265					270						
Lys	Asn	Asp	Glu	Phe	Ile	Arg	Asn	Leu	Phe	Val	Val	Tyr	Gln	Phe	Val				
		275					280					285							
Leu	Arg	Ala	Val	Ala	Lys	Thr	Lys	Arg	Ala	Phe	Leu	Ala	Asn	Ser	Ser				
	290					295					300								
Leu	Tyr	Asn	Ser	Gly	Phe	Asn	Gly	Ala	Ala	Thr	Asp	Gly	Asp	Val	Arg				

Cys Lys Ile Glu Phe Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Arg
115 120 125

Ser Asn Gly Thr Ile Ile His Ile Lys Glu Lys His Leu Cys His Thr
130 135 140

Gln Ser Ser Pro Lys Leu Phe Trp Ala Leu Val Val Val Ala Gly Val
145 150 155 160

Leu Phe Cys Tyr Gly Leu Leu Val Thr Val Ala Leu Cys Val Ile Trp
165 170 175

Thr Asn Ser Arg Arg Asn Arg Leu Leu Gln Val Thr Thr Met Asn Met
180 185 190

Thr Pro Arg Arg Pro Gly Leu Thr Arg Lys Pro Tyr Gln Pro Tyr Ala
195 200 205

Pro Ala Arg Asp Phe Ala Ala Tyr Arg Pro
210 215

<210> 19
<211> 220
<212> PRT
<213> Homo sapiens

<400> 19
Met Leu Arg Leu Leu Leu Ala Leu Asn Leu Phe Pro Ser Ile Gln Val
1 5 10 15

Thr Gly Asn Lys Ile Leu Val Lys Gln Ser Pro Met Leu Val Ala Tyr
20 25 30

Asp Asn Ala Val Asn Leu Ser Cys Lys Tyr Ser Tyr Asn Leu Phe Ser
35 40 45

Arg Glu Phe Arg Ala Ser Leu His Lys Gly Leu Asp Ser Ala Val Glu
50 55 60

Val Cys Val Val Tyr Gly Asn Tyr Ser Gln Gln Leu Gln Val Tyr Ser
65 70 75 80

Lys Thr Gly Phe Asn Cys Asp Gly Lys Leu Gly Asn Glu Ser Val Thr
85 90 95

Phe Tyr Leu Gln Asn Leu Tyr Val Asn Gln Thr Asp Ile Tyr Phe Cys
100 105 110

Lys Ile Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser
115 120 125

Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro
130 135 140

Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly
 145 150 155 160
 Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile
 165 170 175
 Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met
 180 185 190
 Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro
 195 200 205
 Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
 210 215 220

<210> 20
 <211> 223
 <212> PRT
 <213> Mus sp.

<400> 20
 Met Ala Cys Leu Gly Leu Arg Arg Tyr Lys Ala Gln Leu Gln Leu Pro
 1 5 10 15
 Ser Arg Thr Trp Pro Phe Val Ala Leu Leu Thr Leu Leu Phe Ile Pro
 20 25 30
 Val Phe Ser Glu Ala Ile Gln Val Thr Gln Pro Ser Val Val Leu Ala
 35 40 45
 Ser Ser His Gly Val Ala Ser Phe Pro Cys Glu Tyr Ser Pro Ser His
 50 55 60
 Asn Thr Asp Glu Val Arg Val Thr Val Leu Arg Gln Thr Asn Asp Gln
 65 70 75 80
 Met Thr Glu Val Cys Ala Thr Thr Phe Thr Glu Lys Asn Thr Val Gly
 85 90 95
 Phe Leu Asp Tyr Pro Phe Cys Ser Gly Thr Phe Asn Glu Ser Arg Val
 100 105 110
 Asn Leu Thr Ile Gln Gly Leu Arg Ala Val Asp Thr Gly Leu Tyr Leu
 115 120 125
 Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Phe Val Gly Met Gly
 130 135 140
 Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser
 145 150 155 160
 Asp Phe Leu Leu Trp Ile Leu Val Ala Val Ser Leu Gly Leu Phe Phe

Arg Ser Pro Leu Thr Thr Gly Val Tyr Val Lys Met Pro Pro Thr Glu
195 200 205

Pro Glu Cys Glu Lys Gln Phe Gln Pro Tyr Phe Ile Pro Ile Asn
210 215 220

<210> 22

<211> 284

<212> PRT

<213> Caenorhabditis elegans

<400> 22

Met Asn Phe Ile Ser Ala Lys Leu Val Phe Val Pro Trp Leu Trp Asn
1 5 10 15

Lys Met Ala Phe Ile Lys Arg Lys Thr Val Lys Phe Ser Val Asp Leu
20 25 30

Gln Val Cys Gln Leu Ser Asp Val Pro Leu Val Asn Ala Thr Val Phe
35 40 45

Gly Lys Met Arg Leu Leu Asp Gly Gly Ser Phe Glu Glu Ala Thr Glu
50 55 60

Arg Val Glu Glu Gln Lys Gly Gly Lys Ser Tyr Tyr Lys Leu Gly Phe
65 70 75 80

Val Asp Ile Asn Leu Ser Glu Tyr Ala Ala Ser Gly Val Glu Gly Ile
85 90 95

Ser Arg Thr Tyr Leu Leu Asn Gly Tyr Thr Ser Asn Gln Arg Leu Asp
100 105 110

Asn Ser Lys Val Cys Ile Lys Val Ala Met Thr His Gln Ser Ala Asp
115 120 125

Pro Phe Phe Arg Val Pro Arg Leu Ser Thr Phe Gly Pro Arg Gln Asp
130 135 140

Gly Ala Ile Asp Gln Asp Gly Phe Arg Ala Asp Asp Glu Thr Asp Ser
145 150 155 160

Glu Glu Gly Thr Ser Ser His Pro Lys Leu Ser Asn Val Asp Val Leu
165 170 175

Glu Ser Ser Ser Ala Ala Ser Asn Ser Gln Val Asp Glu Pro Val Val
180 185 190

Glu Arg Arg Val Ile His Pro Pro Gln His Pro Thr Cys Gln Leu Arg
195 200 205

Arg Phe Ser Gln Asp Arg Ser Ala Gln Lys Ile Gln His Ser Arg Phe
210 215 220

Asp Ala Asp Asn Val Ile Asp Lys Ile Ile Ala Glu Cys Arg Ile Ser
 225 230 235 240
 Glu Asp Glu Val Glu Ser Asn Ser Gly Gly Leu Val Leu Glu Lys Phe
 245 250 255
 Leu Asp Lys His Gly Lys Pro Leu Val Asn Pro Arg Gln Pro Val Lys
 260 265 270
 Arg Thr Ser Tyr Val Ala Glu His Phe Asn Asp Ala
 275 280

<210> 23
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:oligonucleotide
 primer

<400> 23
 aaccttctag tcctttgggc tgc 23

<210> 24
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 oligonucleotide primer

<400> 24
 ggcccaggct acaggctg 18

099545-12001